CLAIMS:

1. A method for determining predisposition to a physiological reaction of an individual to a biologically active compound comprising characterizing nucleotide sequence of at least one of the *UGT1A1*, *UGT1A7* or *UGT1A9* gene or a part thereof of said individual, wherein the presence of at least one polymorphic or haplotypic variation in said nucleotide sequence is indicative of said predisposition to a physiological reaction.

2. The method of claim 1, wherein said predisposition is a hereditary predisposition.

3. The method of claim 1, wherein said predisposition is a higher or lower susceptibility, sensibility, diathesis, proneness, proclivity, tendency, sensitivity, responsiveness, resistance or constitutional sickness to said physiological reaction.

4. The method of claim 1, wherein said physiological reaction is a beneficial reaction.

5. The method of claim 1, wherein said physiological reaction is an adverse reaction or a side effect.

6. The method of claim 1, wherein said biologically active compound is a xenobiotic.

7. The method of claim 6, wherein said xenobiotic is a drug, a carcinogen or a pre-carcinogen.

8. The method of claim 7, wherein said drug is an anti-cancer agent or an immunosuppressive agent.

9. The method of claim 8, wherein said anti-cancer agent is a camptothecin or an analog thereof.

10. The method of claim 9, wherein said camptothecin analog is 7-ethyl-10-[4-(1-piperidino)-1-piperidino] carbonyloxy camptothecin (irinotecan, CPT-11), 7-ethyl-10-hydroxycamptothecin (SN-38).

11. The method of claim 8, wherein said immunosuppressive agent is mycophenolic acid (MPA).

12. The method of claim 1, wherein said individual is a human or an animal.

13. The method of claim 1, wherein said individual is a patient with cancer.

14. The method of claim 13, wherein said patient has a colorectal cancer or a solid tumor.

15. The method of claim 1, wherein determining genetic sequence is performed on a DNA or a RNA sample.

16. The method of claim 1, wherein said polymorphic or haplotypic variation is a UGT1A9 variation.

17. The method of claim 16, wherein said UGT1A9 variation is at least one of a $C^{-2208}T$ substitution, a $C^{-2152}T$ substitution, a $C^{-2141}T$ substitution, a $T^{-1887}G$ substitution, a $T^{-1818}C$ substitution, a $C^{-665}T$ substitution, a $T^{-440}C$ substitution, a $C^{-331}T$ substitution, a $T^{-275}A$ substitution, a $G^{-87}A$ substitution, a $G^{8}A$ missence mutation ($C^{3}Y$), a $T^{98}C$ missence mutation ($M^{33}T$) or combination thereof.

18. The method of claim 17, wherein said $G^{8}A$ missence mutation is associated with a decreased predisposition or susceptibility to an anti-cancer agent.

19. The method of claim 17, wherein said $G^{8}A$ missence mutation is associated with a decreased responsiveness to an immunosuppressive agent.

20. The method of claim 17, wherein said $T^{98}C$ missence mutation is associated with an increased adverse reaction to an anti-cancer agent.

21. The method of claim 1, wherein said polymorphic or haplotypic variation is a UGT1A7 variation.

22. The method of claim 21, wherein said UGT1A7 variation is a $G^{353}T$ missense mutation, a $T^{397}G$ missense mutation, a $C^{401}A$ missense mutation, a $G^{402}A$ missense mutations, a $G^{427}C$ missense mutation, a $T^{632}C$ missense mutation or combination thereof.

23. The method of claim 1, wherein said polymorphic or haplotypic variation is a UGT1A1 variation.

24. The method of claim 23, wherein said UGT1A1 variation is a TA_7 mutation in the TATA box.

25. An isolated nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45 SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, a fragment or the complementary sequences thereof, for determining predisposition to a physiological reaction.

26. The nucleotide sequence of claim 25, wherein said sequence is an allelic variant of UGT1A1, UGT1A7 or UGT1A9.

27. An isolated amino acid sequence comprising at least one amino acid sequence selected from the group consisting of SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71 or a fragment thereof.

28. The amino acid sequence of claim 27, wherein said sequence is encoded by a nucleotide sequence comprising at least one sequence selected from the group consisting of SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, a fragment or the complementary sequences thereof.

29. The amino acid sequence of claim 27, wherein the expression of said sequence is regulated by a nucleotide sequence comprising at least one sequence selected from the group consisting of SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45 SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, a fragment or the complementary sequences thereof.